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OM protein - protein search, using sw model

Run on: December 24, 2002, 09:16:46 ; Search time 91 Seconds  
(Without alignments)  
26.357 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87

Sequence: 1 ALYKKFKKLKSLKRLG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*

2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*

3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*

4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*

5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*

6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*

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9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*

10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*

11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*

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19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*

20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*

21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*

22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	18	20	AAV57465
2	87	100.0	19	20	AAV57469
3	87	100.0	19	20	AAV57501
4	87	100.0	20	20	AAV57502
5	87	100.0	25	20	AAV57496
6	87	100.0	35	20	AAV57497
7	83	95.4	18	20	AAV57504
8	82	94.3	18	20	AAV57500
9	81	93.1	18	20	AAV57503
10	77	88.5	18	20	AAV57505

11	66	75.9	18	12	AAV57465	standard: Peptide: 18 AA.
12	66	75.9	18	18	AAV57465	
13	66	75.9	18	21	AAV57465	
14	66	75.9	19	18	AAV57465	
15	66	75.9	19	21	AAV57465	
16	64	73.6	18	20	AAV57465	
17	62	71.3	18	12	AAV57465	
18	62	71.3	18	12	AAV57465	
19	62	71.3	20	12	AAV57465	
20	62	71.3	23	12	AAV57465	
21	61	70.1	18	12	AAV57465	
22	57	65.5	13	20	AAV57465	
23	56	64.4	18	12	AAV57465	
24	53	60.9	13	20	AAV57465	
25	52	59.8	18	20	AAV57465	
26	52	59.8	39	15	AAV57465	
27	52	59.8	39	15	AAV57465	
28	50	57.5	14	20	AAV57465	
29	48	55.2	18	13	AAV57465	
30	48	55.2	18	13	AAV57465	
31	48	55.2	18	13	AAV57465	
32	47	54.0	13	20	AAV57465	
33	47	54.0	14	20	AAV57465	
34	47	54.0	18	12	AAV57465	
35	46	52.9	18	13	AAV57465	
36	46	52.9	18	13	AAV57465	
37	46	52.9	18	13	AAV57465	
38	46	52.9	18	13	AAV57465	
39	46	52.9	18	13	AAV57465	
40	46	52.9	46	19	AAV57465	
41	46	52.9	46	20	AAV57465	
42	45	51.7	13	20	AAV57465	
43	45	51.7	16	16	AAV57465	
44	45	51.7	16	16	AAV57465	
45	45	51.7	17	16	AAV57465	

## ALIGNMENTS

RESULT 1	AAV57465	standard: Peptide: 18 AA.
ID	AAV57465	
XX	AAV57465	
AC	AAV57465	
XX	AAV57465	
DT	25-FEB-2000 (first entry)	
XX	Antimicrobial peptide RP-1 SEQ ID NO:3.	
DE	Antimicrobial peptide: metapeptide: PMR-2; platelet microbicidal protein:	
KW	antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.	
XX	Synthetic.	
OS	Oryctolagus cuniculus.	
XX	WO9942119-A1.	
PN	26-AUG-1999.	
XX	17-FEB-1999: 99WO-US03350.	
PF	18-FEB-1998: 98US-0025319.	
XX	(HARB-) HARBOR-UCLA RES & EDUCATION INST.	
PA	Yeaman MR, Shen AJ;	
XX	WPI: 1999-527417/44.	
DR	Antimicrobial peptides for potentiating antimicrobial agents active	
XX	against bacteria and fungi	
PT		
XX		

PS Claim 17; Page 106; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZBXXB and its derivatives  
 CC selected from XZBVBXXB, BXZXB, BXZXXB, XBBXXZBXX and BXZBXXZ;  
 CC (b) a second peptide template XBBXX and their derivatives selected from  
 CC the group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBZXXB, and  
 CC XBBZXXBXXZBXX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 18 AA:

Query Match 100.0%; Score 87; DB 20; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKLKSLKRLG 18  
 DB 1 ALYKFKKKLKLKSLKRLG 18

RESULT 2  
 AAY57499  
 ID AAY57499 standard; Peptide: 19 AA.

XX AC AAY57499;  
 XX DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.  
 OS Oryctolagus cuniculus.

XX PA WO9942119-A1.  
 XX PN 26-AUG-1999.  
 XX DR 17-FEB-1999; 99WO-US03350.  
 XX PF 18-FEB-1998; 98US-0025319.  
 XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;  
 XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active  
 XX PT against bacteria and fungi

XX PS Disclosure; Page 58; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZBXXB and its derivatives  
 CC selected from XZBVBXXB, BXZXB, BXZXXB, XBBXXZBXX and BXZBXXZ; and  
 CC (b) a second peptide template XBBXX and their derivatives selected from  
 CC the group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBZXXB, and

CC XBBZXXBXXZBXX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 19 AA:

Query Match 100.0%; Score 87; DB 20; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKLKSLKRLG 18  
 DB 2 ALYKFKKKLKLKSLKRLG 19

RESULT 3  
 AAY57501  
 ID AAY57501 standard; Peptide: 19 AA.

XX AC AAY57501;  
 XX DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.  
 OS Oryctolagus cuniculus.

XX PA WO9942119-A1.  
 XX PN 26-AUG-1999.  
 XX DR 17-FEB-1999; 99WO-US03350.  
 XX PF 18-FEB-1998; 98US-0025319.  
 XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;  
 XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active  
 XX PT against bacteria and fungi

XX PS Disclosure; Page 59; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZBXXB and its derivatives  
 CC selected from XZBVBXXB, BXZXB, BXZXXB, XBBXXZBXX and BXZBXXZ; and  
 CC (b) a second peptide template XBBXX and their derivatives selected from  
 CC the group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBZXXB, and  
 CC XBBZXXBXXZBXX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 19 AA:

Query Match 100.0%; Score 87; DB 20; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKLKSLKRLG 18  
 |||||  
 DB 1 ALYKFKKKLKLKSLKRLG 18

RESULT 4  
 AAY57502  
 ID AAY57502 standard; Peptide: 20 AA.  
 AC AAY57502;  
 XX  
 DT 25-FEB-2000 (first entry)  
 XX  
 DE Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.  
 XX  
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.  
 XX  
 OS Synthetic.  
 OS Oryctolagus cuniculus.  
 XX  
 PN WO9942119-A1.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 17-FEB-1999; 99WO-US03350.  
 XX  
 PR 18-FEB-1998; 98US-0025319.  
 XX  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ;  
 XX  
 DR WPI; 1999-527417/44.  
 XX  
 PT Antimicrobial peptides for potentiating antimicrobial agents active  
 PT against bacteria and fungi  
 PS Disclosure; Page 59; 166pp; English.  
 XX  
 CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZBXXB and its derivatives  
 CC selected from XZBZBXXB, BXZXB, BXZXZXB, XBBXXZBXX and BXZBXXZ; and  
 CC (b) a second peptide template XBBXX and their derivatives selected from  
 CC the group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBXXBB, and  
 CC XBBZXBBXXZBXX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SO Sequence 20 AA:

Query Match 100.0%; Score 87; DB 20; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKLKSLKRLG 18  
 |||||  
 DB 2 ALYKFKKKLKLKSLKRLG 19

RESULT 5  
 AAY57496  
 ID AAY57496 standard; Peptide: 25 AA.  
 AC AAY57496;  
 XX  
 DT 25-FEB-2000 (first entry)  
 XX  
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.  
 XX  
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.  
 XX  
 OS Synthetic.  
 OS Oryctolagus cuniculus.  
 XX  
 PN WO9942119-A1.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 17-FEB-1999; 99WO-US03350.  
 XX  
 PR 18-FEB-1998; 98US-0025319.  
 XX  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ;  
 XX  
 DR WPI; 1999-527417/44.  
 XX  
 PT Antimicrobial peptides for potentiating antimicrobial agents active  
 PT against bacteria and fungi  
 PS Disclosure; Page 126; 166pp; English.  
 XX  
 CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XZBZBXXB and its derivatives  
 CC selected from XZBZBXXB, BXZXB, BXZXZXB, XBBXXZBXX and BXZBXXZ; and  
 CC (b) a second peptide template XBBXX and their derivatives selected from  
 CC the group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBXXBB, and  
 CC XBBZXBBXXZBXX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SO Sequence 25 AA:

Query Match 100.0%; Score 87; DB 20; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKLKSLKRLG 18  
 |||||  
 DB 1 ALYKFKKKLKLKSLKRLG 18

RESULT 6  
 AAY57497  
 ID AAY57497 standard; Peptide: 35 AA.  
 AC AAY57497;  
 XX  
 DT 25-FEB-2000 (first entry)  
 XX  
 DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.  
 XX

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.  
 OS Synthetic.  
 OS Oryctolagus cuniculus.  
 PM MO9942119-A1.  
 PD 26-AUG-1999.  
 PF 17-FEB-1999; 99WO-US03350.  
 PR 18-FEB-1998; 98US-0025319.  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ.  
 DR WPI: 1999-527417/44.  
 XX Antimicrobial peptides for potentiating antimicrobial agents active  
 PT against bacteria and fungi -  
 PS Disclosure; Page 126; 166pp; English.  
 CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XBZBXBXB and its derivatives  
 CC selected from XBZBXBXB, BXZXB, BXZXZXB, XBZBXBXB and BXZBXBXZ; and  
 CC (b) a second peptide template XBZBXBXB and their derivatives selected from  
 CC the group consisting of XBZBXBXB, XBZBXBXB, BXZBXBXB, and  
 CC XBZBXBXBXZBX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 CC XX  
 SQ Sequence 35 AA;  
 Query Match 100.0%; Score 87; DB 20; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALYKFKKKLKLKSLKRLG 18  
 Db 1 ALYKFKKKLKLKSLKRLG 18  
 RESULT 7  
 AAY57504  
 ID AAY57504 standard; Peptide: 18 AA.  
 AC AAY57504;  
 XX  
 DT 25-FEB-2000 (first entry)  
 DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.  
 DE XX  
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.  
 OS Synthetic.  
 OS Oryctolagus cuniculus.  
 PM MO9942119-A1.  
 PD 26-AUG-1999.  
 PF 17-FEB-1999; 99WO-US03350.  
 PR 18-FEB-1998; 98US-0025319.  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ.  
 DR WPI: 1999-527417/44.

PF 17-FEB-1999; 99WO-US03350.  
 XX  
 PR 18-FEB-1998; 98US-0025319.  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ.  
 DR WPI: 1999-527417/44.  
 XX Antimicrobial peptides for potentiating antimicrobial agents active  
 PT against bacteria and fungi -  
 PS Disclosure; Page 59; 166pp; English.  
 CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XBZBXBXB and its derivatives  
 CC selected from XBZBXBXB, BXZXB, BXZXZXB, XBZBXBXB and BXZBXBXZ; and  
 CC (b) a second peptide template XBZBXBXB and their derivatives selected from  
 CC the group consisting of XBZBXBXB, XBZBXBXB, BXZBXBXB, and  
 CC XBZBXBXBXZBX; where B = at least one positively charged amino acid;  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 CC XX  
 SQ Sequence 18 AA;  
 Query Match 95.4%; Score 83; DB 20; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 2.9e-05;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ALYKFKKKLKLKSLKRLG 18  
 Db 1 ALYKFKKKLKLKSLKRLG 18  
 RESULT 8  
 AAY57500  
 ID AAY57500 standard; Peptide: 18 AA.  
 AC AAY57500;  
 XX  
 DT 25-FEB-2000 (first entry)  
 DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.  
 DE XX  
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;  
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.  
 OS Synthetic.  
 OS Oryctolagus cuniculus.  
 PM MO9942119-A1.  
 PD 26-AUG-1999.  
 PF 17-FEB-1999; 99WO-US03350.  
 PR 18-FEB-1998; 98US-0025319.  
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
 PI Yeaman MR, Shen AJ.  
 DR WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active  
 XX against bacteria and fungi  
 PS Disclosure: Page 58; 16pp; English.  
 CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XBRZXBXB and its derivatives  
 CC selected from XBRZXBXB, BXZXB, BXZXB, XBRZXB and BXZXB; and  
 CC (b) a second peptide template XBBXB, BXBBXB, BXBBXB, and  
 CC the group consisting of XBBXB, BXBBXB, BXBBXB, and  
 CC XBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, and  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 SQ Sequence 18 AA:

Query Match 94.3%; Score 82; DB 20; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 4.1e-05;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKSLKRLG 18  
 | | | | | | | | | | | | | | | | | |  
 Db 1 ALYKFKKKLKSLKRLG 18

RESULT 9  
 AAY57503  
 ID AAY57503 standard; Peptide: 18 AA.

XX AAY57503;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.

KM Antimicrobial; metaprotein; PMP-2; platelet microbicidal protein;

XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active

PS against bacteria and fungi  
 Disclosure: Page 59; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XBRZXBXB and its derivatives

CC selected from XBRZXBXB, BXZXB, BXZXB, XBRZXB and BXZXB; and  
 CC (b) a second peptide template XBBXB and their derivatives selected from  
 CC the group consisting of XBBXB, BXBBXB, BXBBXB, BXBBXB, and  
 CC XBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, and  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent  
 CC sequences used in the exemplification of the present invention.  
 SQ Sequence 18 AA:

Query Match 93.1%; Score 81; DB 20; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 5.7e-05;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKSLKRLG 18  
 | | | | | | | | | | | | | | | | | |  
 Db 1 ALYKFKKKLKSLKRLG 18

RESULT 10  
 AAY57505  
 ID AAY57505 standard; Peptide: 18 AA.

XX AAY57505;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.

KM Antimicrobial; metaprotein; PMP-2; platelet microbicidal protein;

XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active

PS against bacteria and fungi  
 Disclosure: Page 59; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct  
 CC activity or for potentiating antimicrobial agents active against  
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide  
 CC containing an amino acid sequence selected from the group consisting  
 CC essentially of a first peptide template XBRZXBXB and its derivatives  
 CC selected from XBRZXBXB, BXZXB, BXZXB, XBRZXB and BXZXB; and  
 CC (b) a second peptide template XBBXB and their derivatives selected from  
 CC the group consisting of XBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, and  
 CC XBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, BXBBXB, and  
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one  
 CC aromatic amino acid, and where B, X and Z may be separated by one or  
 CC more other amino acids. The peptides can be used to treat bacterial and  
 CC fungal infections. The peptides also increase the antimicrobial activity  
 CC of neutrophils. The peptides overall effect cellular disruption and  
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent

CC sequences used in the exemplification of the present invention.  
XX

SO Sequence 18 AA;

Query Match 88.5%; Score 77; DB 20; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.00021;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKSLKRLG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 ARYKFKKKFLKSLKRLG 18

# RESULT 11

AAR13927 standard; Protein; 18 AA.

XX AAR13927;

XX 26-NOV-1991 (first entry)

XX Cationic oligopeptide #3.

XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.

XX Synthetic.

XX WO9112815-A.

XX 05-SEP-1991.

XX 25-FEB-1991; 91WO-US01224.

XX 19-FEB-1991; 91US-0655321.

XX 23-FEB-1990; 90US-0484020.

XX (BRIM) BRISTOL-MYERS SQUIB.

XX Darveau RP, Blake JJ, Cosand WL;

XX WPI; 1991-281214/38.

XX Comps. for treating infections sensitive to beta-lactam

XX antibiotics - comprise beta-lactam antibiotic and cationic

XX oligopeptide, useful against Enterobacteriaceae, Pseudomonas

XX aeruginosa etc.

XX Claim 17; Page 44; 64pp; English.

XX This is a specific example of a cationic oligopeptide suitable for

XX use in compositions with beta-lactam antibiotics. The peptide has

XX an alpha-helical structure and is believed to act as an ionophore,

XX making holes in bacterial cell membranes. The peptide and antibiotic

XX act synergistically. See AAR13924-R13930 and AAR13936-7.

XX Sequence 18 AA:

OY 1 ALYKFKKKLKSLKRLG 18

Db 1 ALYKFKKKLKSLKRLG 18

XX 11-APR-2000 (first entry)

XX 22-SEP-1997 (first entry)

XX Antibacterial peptide C18G for immunoadapter synthesis.

XX Antimicrobial: immunoglobulin; surface binding ligand;

XX hapten; sepsis; influenza; viremia; fungemia; neurology; cancer;

XX endocrinology; antidiabetic; antibody; antibiotic.

XX Synthetic.

XX WO9640251-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US10227.

XX 07-JUN-1995; 95US-0482191.

XX (OPHI-) OPHIDIAN PHARM INC.

XX Firca JR, Panasik N, Pugh C, Schatz RW, Shekhani MS;

XX Stafford D, Williams JA;

XX WPI; 1997-077224/07.

XX Example 39; Page 150; 227pp; English.

XX The present sequence is an antibacterial peptide C18G, which was

XX modified by adding a Cys-amide to the carboxy terminus. This was used to

XX produce an immunoadapter conjugate. Making a conjugate comprises

XX covalently linking a surface-binding ligand (SBL) to a hapten via a

XX spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the

XX compound with immunoglobulin (Ig) under conditions that allow for non-

XX covalent binding of the Ig to the hapten of the compound. The conjugate

XX can be used for the diagnosis, prevention and treatment of microbial

XX infections, e.g. sepsis, influenza, viremia or fungemia. They can also

XX be used in neurology, cancer and endocrinology, where Ig targeting can

XX provide desired therapeutic effects. The methods for producing a

XX conjugate can use small molecule targeting ligands to efficiently

XX direct otherwise unreactive Ig to microbial targets. This targeting

XX allows Ig to react with microbial structures that may not normally be

XX accessible to Ig, or are incapable of stimulating antibody production.

XX Sequence 18 AA:

OY 1 ALYKFKKKLKSLKRLG 18

Db 1 ALYKFKKKLKSLKRLG 18

XX 11-APR-2000 (first entry)

XX 22-SEP-1997 (first entry)

XX US5998381-A.

XX US5998381-A.

XX 07-DEC-1999.  
 PD 06-DEC-1996; 96DS-0760903.  
 XX 06-DEC-1996; 96DS-0760903.  
 PR 06-DEC-1996; 96DS-0760903.  
 XX (OPHI-) OPHIDIAN PHARM INC.  
 PA Shekhan MS, Anderson B, Firca JR;  
 PI WPI: 2000-115173/10.  
 DR  
 XX  
 XX  
 PT Therapeutic formulation comprising  
 PT N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl  
 PT derivative useful for diagnosing and treating bacterial diseases -  
 XX  
 PS Example 39; Column 84; 89pp; English.

CC The present invention describes a therapeutic formulation comprising  
 CC N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also  
 CC described is a method of treatment for bacterial disease comprising:  
 CC (a) providing a subject with symptoms of bacterial disease with one or  
 CC more fimbriae-binding compounds comprising a mannose of an anomer  
 CC configuration, an alpha-aromatic or heteroaromatic ring attached to the  
 CC mannose by a glycosidic or pseudoglycosidic linkage and a functional  
 CC group which provides a site for chemical modification remote from the  
 CC mannose and a pharmaceutically carrier; and (b) administering the  
 CC fimbriae-binding compound to the subject. Administration of one or more  
 CC fimbriae-binding compounds can be used for treating subjects with  
 CC symptoms of and for subjects at risk from bacterial diseases. Treatment  
 CC of and prevention of blood-borne and toxin mediated diseases in  
 CC particular sepsis in humans and other animals can be carried out and the  
 CC in vivo neutralisation of the effects of endotoxin is also possible.  
 CC The compounds may also be used to identify bacteria according to their  
 CC cell binding specificity's through conjugation to reporter substances  
 CC such as dyes, luminescent or fluorescent molecules and enzymes. The  
 CC compounds also inhibit the agglutination of yeast cells induced by type  
 CC 1 pilli bearing bacteria. The present sequence is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 18 AA:

Query Match 75.9%; Score 66; DB 21; Length 18;  
 Best Local Similarity 77.8%; Pred. No. 0.0076;  
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLKSLKRLG 18  
 ||||| ||||| :||  
 DB 1 ALYKLLKLLKLSAKKLG 18

RESULT 14

AAW10352  
 ID AAW10352 standard; peptide: 19 AA.

AC AAW10352;

DT 22-SEP-1997 (first entry)

DE Antibacterial peptide C19G for immunoadapter synthesis.

XX Antimicrobial; immunoglobulin; surface binding ligand;

KW haptens; sepsis; influenza; viremia; fungemia; neurology; cancer;

KW endocrinology; antibacterial; antibody; antibiotic.

OS Synthetic.

XX Key

FN Modified-site 19

PN W09640251-A1.

XX 19-DEC-1996.  
 PD 07-JUN-1996; 96WO-US10227.  
 XX 07-JUN-1996; 96WO-US10227.  
 PR 07-JUN-1996; 96WO-US10227.  
 XX (OPHI-) OPHIDIAN PHARM INC.  
 PA Firca JR, Panasik N, Pugh C, Schatz RW, Shekhan MS;  
 PI Stafford D, Williams JA;  
 DR WPI: 1997-077224/07.  
 XX  
 XX  
 PT Antimicrobial compns. for diagnosis and therapy - comprising  
 PT microbial surface binding ligand-spacer-hapten, non-covalently  
 PT associated with immunoglobulin

PS Example 39; Page 150; 227pp; English.

CC The present sequence is a peptide designated C19G. This was used to  
 CC produce an immunoadapter conjugate. Making a conjugate comprises  
 CC covalently linking a surface-binding ligand (SBL) to a hapten via a  
 CC spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the  
 CC compound with immunoglobulin (Ig) under conditions that allow for non-  
 CC covalent binding of the Ig to the hapten of the compound. The conjugate  
 CC can be used for the diagnosis, prevention and treatment of microbial  
 CC infections, e.g. sepsis, influenza, viremia or fungemia. They can also  
 CC be used in neurology, cancer and endocrinology, where Ig targeting can  
 CC provide desired therapeutic effects. The methods for producing a  
 CC conjugate can use small molecule targeting ligands to efficiently  
 CC direct otherwise unreactive Ig to microbial targets. This targeting  
 CC allows Ig to react with microbial structures that may not normally be  
 CC accessible to Ig, or are incapable of stimulating antibody production.

XX SQ Sequence 19 AA:

Query Match 75.9%; Score 66; DB 18; Length 19;  
 Best Local Similarity 77.8%; Pred. No. 0.008;  
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLKSLKRLG 18  
 ||||| ||||| :||  
 DB 1 ALYKLLKLLKLSAKKLG 18

RESULT 15

AAV68002  
 ID AAV68002 standard; peptide: 19 AA.

AC AAV68002;

DT 11-APR-2000 (first entry)

DE Antibacterial peptide C19G SEQ ID NO:3.

XX Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;

KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

OS Synthetic.

XX US5998381-A.

PD 07-DEC-1999.

PF 06-DEC-1996; 96DS-0760903.

PR 06-DEC-1996; 96DS-0760903.

PA (OPHI-) OPHIDIAN PHARM INC.  
 PI Shekhan MS, Anderson B, Firca JR;

DR WPI: 2000-115173/10.

XX Therapeutic formulation comprising  
 PT N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl  
 PT derivative useful for diagnosing and treating bacterial diseases -

XX Example 39: Column 84: 89pp: English.

PS  
 CC The present invention describes a therapeutic formulation comprising  
 CC N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also  
 CC described is a method of treatment for bacterial disease comprising:  
 CC (a) providing a subject with symptoms of bacterial disease with one or  
 CC more fimbriae-binding compounds comprising a mannose of an anomeric  
 CC configuration, an alpha-aromatic or heteroaromatic ring attached to the  
 CC mannose by a glycosidic or pseudoglycosidic linkage and a functional  
 CC group which provides a site for chemical modification remote from the  
 CC mannose and a pharmaceutically carrier; and (b) administering the  
 CC fimbriae-binding compound to the subject. Administration of one or more  
 CC fimbriae-binding compounds can be used for treating subjects with  
 CC symptoms of and for subjects at risk from bacterial diseases. Treatment  
 CC of and prevention of blood-borne and toxin mediated diseases in  
 CC particular sepsis in humans and other animals can be carried out and the  
 CC in vivo neutralisation of the effects of endotoxin is also possible.  
 CC The compounds may also be used to identify bacteria according to their  
 CC cell binding specificity's through conjugation to reporter substances  
 CC such as dyes, luminescent or fluorescent molecules and enzymes. The  
 CC compounds also inhibit the agglutination of yeast cells induced by type  
 CC 1 pill bearing bacteria. The present sequence is used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 19 AA;

Query Match 75.9%; Score 66; DB 21; Length 19;

Best Local Similarity 77.8%; Pred. No. 0.008;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKFKKLLKSLKRLG 18  
 ||||| ||||| :||  
 DB 1 ALYKRLKLLKLSAKKLG 18

Search completed: December 24, 2002, 09:18:27  
 Job time : 92 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2002, 09:16:51 : Search time 55 Seconds  
(without alignments)  
31.462 Million cell updates/sec

Title: US-09-648-816b-3

Perfect score: 87

Sequence: 1 ALYKKFKKKLLKSLKRLG 18

Scoring table: BL0SUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	58.6	487	2	C64470
2	48	55.2	540	2	A70358
3	47	54.0	139	2	H75179
4	46	52.9	399	2	S70634
5	46	52.9	472	2	B90095
6	46	52.9	733	2	T49679
7	45	51.7	90	2	S69133
8	45	51.7	140	2	H71033
9	45	51.7	160	2	T33883
10	45	51.7	187	2	AH1489
11	45	51.7	427	2	S38002
12	45	51.7	568	2	UC5923
13	45	51.7	569	2	S51685
14	44.5	51.1	615	2	E86212
15	44	50.6	192	2	F35270
16	44	50.6	254	2	F90087
17	44	50.6	266	2	B90286
18	44	50.6	729	2	T41735
19	44	50.6	778	2	T17679
20	44	50.6	828	2	S56250
21	43.5	50.0	642	2	T39376
22	43	49.4	239	2	S59050
23	43	49.4	398	2	T27670
24	43	49.4	425	2	B64316
25	43	49.4	497	2	E90061
26	43	49.4	727	2	AD1868
27	42.5	48.9	141	2	T28192
28	42	48.3	427	2	E64644
29	42	48.3	436	2	S47628

## ALIGNMENTS

30	42	48.3	488	1	139769	aldehyde dehydroge
31	42	48.3	558	2	T47508	probable transport
32	42	48.3	559	2	T42646	hypothetical prote
33	42	48.3	704	1	S50448	1,4-alpha-glucan b
34	42	48.3	1165	2	A70423	valine-tRNA ligase
35	41	47.1	76	2	G81882	hypothetical prote
36	41	47.1	101	1	PFH04	hypothetical factor
37	41	47.1	105	2	A26774	platelet factor 4
38	41	47.1	109	2	T27847	platelet factor 4
39	41	47.1	118	2	T27846	hypothetical prote
40	41	47.1	143	2	B90523	hypothetical prote
41	41	47.1	153	2	A55139	hypoglycin, body wa
42	41	47.1	203	2	JC7163	hepatoma-derived g
43	41	47.1	211	2	T01194	hypothetical prote
44	41	47.1	221	2	F84960	membrane-bound lgt
45	41	47.1	248	2	AF2111	heat shock protein

## RESULT 1

C64470  
hypothetical protein MJ1364 - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: C64470  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak  
reson, J.D.; Sadow, P.W.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: C64470  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Residues: 1-487 <BUI>  
A:Cross-references: GB:067576; GB:177117; NID:g2826398; PIDN:AAB99372.1; PID:g1592008  
C:Genetics:  
A:Map position: FOR1313161-1314624  
A:Start codon: TTG

## Query Match

Best Local Similarity 58.6%; Score 51; DB 2; Length 487;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKKFKKKLLKSLKR 16

Db 264 YKKSEKKLIKDLKR 277

## RESULT 2

A70358  
topoisomerase I - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999

C:Accession: A70358

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: A70358

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-540 <AQF>

A:Cross-references: GB:AE000700; NID:g2983248; PIDN:AAC06848.1; PID:g2983253; GB:AE00

A:Experimental source: strain VFS

C:Genetics:

A:Gene: topA

## Query Match

55.2%; Score 48; DB 2; Length 540;

Best Local Similarity 56.2%; Pred. No. 20;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKFKKKLLSKRL 17  
|||:||||:|:|  
DB 52 YKRGKKLLVQQLKL 67

## RESULT 3

H75179  
hypothetical protein PAB2413 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 28-Jul-2000

C:Accession: H75179  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: H75179  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-139 <KAM>  
A:Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49519.1; PID:9545802  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB2413  
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB2413

Query Match 54.0%; Score 47; DB 2; Length 139;  
Best Local Similarity 44.4%; Pred. No. 8;  
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKFKKKLLSKRLG 18  
|||:||||:|:|  
DB 60 SLVFKVSKVLRALEOMG 77

## RESULT 4

S70634  
translational elongation factor eEF-1 alpha chain - Hexamita sp. (strain ATCC 50330) (frag

C:Species: Hexamita sp.  
A:Variety: ATCC 50330  
C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-Dec-1999

C:Accession: S70634  
R:Keeling, P.J.; Doolittle, W.F.  
EMBO J. 15, 2285-2290, 1996  
A:Title: A non-canonical genetic code in an early diverging eukaryotic lineage.  
A:Reference number: S70634; MUID:96208514; PMID:8641293  
A:Accession: S70634  
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA  
A:Residues: 1-399 <KEE>  
A:Cross-references: EMBL:U294442; NID:91322215; PIDN:AAC47211.1; PID:91322216  
A:Experimental source: ATCC 50330  
C:Genetics:  
A:Genetic code: SGC5  
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo  
C:Keywords: GTP binding; protein biosynthesis

Query Match 52.9%; Score 46; DB 2; Length 399;  
Best Local Similarity 44.4%; Pred. No. 30;  
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKFKKKLLSKRLG 18  
|||:||||:|:|  
DB 148 ARYKEIKEMQKLNKOIG 165

## RESULT 5

B90095  
hypothetical protein orf472 [imported] - Guillardia theta nucleomorph

C:Species: nucleomorph Guillardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001

C:Accession: B90095  
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.;  
Nature 410, 1091-1096, 2001  
A:Title: The highly reduced genome of an enslaved algal nucleus.  
A:Reference number: A90082; MUID:11323671; PMID:11323671  
A:Accession: B90095

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-472 <DOO>  
A:Cross-references: GB:AF165018; NID:913794515; PIDN:AAK39890.1; GSPDB:GN00150  
C:Genetics:  
A:Gene: orf472  
A:Map position: 1  
A:genome: nucleomorph  
C:Keywords: nucleomorph

Query Match 52.9%; Score 46; DB 2; Length 472;  
Best Local Similarity 64.3%; Pred. No. 35;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 KFKKKLLSKRL 17  
|||:||||:|:|  
DB 256 KTKKKLLNSLKKI 269

## RESULT 6

T49679  
probable branching enzyme (bel) [imported] - Neurospora crassa

N:Alternate names: protein B8B20.330  
C:Species: Neurospora crassa  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000

C:Accession: T49679  
R:Schulte, U.; Align, V.; Hohnsels, J.; Brandt, P.; Farthmann, B.; Holland, R.; Nyakatu  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022  
A:Accession: T49679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-733 <SCH>  
A:Cross-references: EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.330  
A:Experimental source: BAC clone B8B20; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B8B20.330  
A:Map position: 6  
A:introns: 30/2; 74/3; 108/1; 146/3; 377/2; 489/2; 701/1  
C:Superfamily: 1,4-alpha-glucan branching enzyme

Query Match 52.9%; Score 46; DB 2; Length 733;  
Best Local Similarity 50.0%; Pred. No. 53;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 ALYKFKKKLLSKRLG 18  
|||:||||:|:|  
DB 220 ATYKEFKTMLPRKIMG 237

## RESULT 7

S69133  
platelet factor 4 - pig

C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 07-May-1999  
C:Accession: S69133  
R:Proudfoot, A.E.I.; Magnenat, E.; Haley, T.M.; Malone, T.E.; Wells, T.N.C.  
Eur. J. Biochem. 228, 658-664, 1995  
A:Title: The complete primary structure of glycosylated porcine platelet factor 4.  
A:Reference number: S69133; MUID:95255268; PMID:7737160  
A:Accession: S69133  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-90 <PRO>  
A:Note: blocked N-terminus  
C:Superfamily: beta-thromboglobulin

Query Match 51.7%; Score 45; DB 2; Length 90;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKFKKKLKLS 13  
DB 74 LYKFKKKLKLS 85

## RESULT 8

hypothetical protein PH1560 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 28-Jul-2000  
C:Accession: H71033

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuji, Y.; Fuchishashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: H71033

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1140 <KAW>

A:Cross-references: GB:AP000006; NID:g3236133; PIDN:BA30672.1; PID:g3257989

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1560  
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB2413

Query Match 51.7%; Score 45; DB 2; Length 140;  
Best Local Similarity 38.9%; Pred. No. 16;  
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKSLKRG 18  
DB 60 SLTPKVSCKVMRALEQMG 77

## RESULT 9

hypothetical protein H14E04.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33883

R:Becker, M.; Wamsley, P.; Twyman, B.; Beck, C.; Bradshaw, H.  
submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid H14E04.  
A:Reference number: Z21431

A:Accession: T33883

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-160 <BEC>

A:Cross-references: EMBL:AF152448; PIDN:ADD12811.1; GSPDB:GN00022; CESP:H14E04.4

A:Experimental source: strain Bristol N2; clone H14E04

C:Genetics:

A:Gene: CESP:H14E04.4

A:Map position: 4

A:introns: 22/3; 36/1; 75/3; 136/2

Query Match 51.7%; Score 45; DB 2; Length 160;  
Best Local Similarity 50.0%; Pred. No. 18;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 YKFKKKLKSLKRG 18  
DB 111 FQFSSKKFLKLNKNG 126

## RESULT 10

AH1489

hypothetical protein lin0456 [imported] - Listeria innocua (strain Clp11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AH1489  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,  
D.; Jones, L.M.; Karst, U  
Science 294, 849-852, 2001  
A:Authors: Kreil, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madeno, E.; Maitournam, A.;  
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1489

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-187 <GLA>

A:Cross-references: GB:AU592022; PIDN:CAC95688.1; PID:g16412897; GSPDB:GN00178

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin0456

Query Match 51.7%; Score 45; DB 2; Length 187;  
Best Local Similarity 46.7%; Pred. No. 21;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKFKKKLKSLKLR 16  
DB 171 LYKFKKKRLVNNYKR 185

hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YKL636  
C:Species: Saccharomyces cerevisiae  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 19-Apr-2002  
C:Accession: S38002; S44589; S38409

R:Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the Protein Sequence Database, March 1994

A:Reference number: S37976

A:Accession: S38002

A:Molecule type: DNA

A:Residues: 1-427 <VAN>

A:Cross-references: EMBL:Z28172; NID:g486301; PIDN:CAA82014.1; PID:g486302; MIPS:YKL1

A:Experimental source: strain S288C

R:Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
Yeast 10, 25-33, 1994

A:Title: Sequencing and analysis of a 20.5 kb DNA segment located on the left arm of

A:Reference number: S44583

A:Accession: S44589

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-427 <VA2>

A:Cross-references: EMBL:Z26878; NID:g407503; PIDN:CAA81515.1; PID:g407510

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:EBP2

A:Cross-references: SGD:S0001655

A:Map position: 11L

Query Match 51.7%; Score 45; DB 2; Length 427;  
Best Local Similarity 58.8%; Pred. No. 45;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKFKKKLKSLKRL 17  
DB 75 ALSKREKKRLKELKLM 91

## RESULT 12

JC5923

sphingosine-1-phosphate lyase (EC 4.-.-.-) [validated] - mouse  
C:Species: Mus musculus (house mouse)

```
C:Genetics:
A:Map position: 1
C:Superfamily: tomato leucine zipper-containing protein

Query Match          51.18;   Score 44.5;   DB 2;   Length 615;
Best Local Similarity 50.08;   Pred. No. 75;
Matches      9;   Conservative      3;   Indels      1;   Gaps      1;

OY      2    LYKFKKKLL-KSLKRLG 18
         |||||::: : | ||
Db       199  IYKFKRKKLIIVDTLSHLG 216

RESULT 15
F35270
pyruvate kinase (EC 2.7.1.40) - Spiroplasma citri (fragment)
C:Species: Spiroplasma citri
C>Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 07-Dec-1999
C:Accession: F35270
R:Chevalier, C.; Sallard, C.; Boye, J.M.
J. Bacteriol. 172, 2693-2703, 1990
A:title: Organization and nucleotide sequences of the Spiroplasma citri genes for rib
in.
A:Reference number: A35270; MUID:90236934; PMID:2139649
A:Accession: F35270
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <CHE>
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: pyruvate kinase
C:key words: phosphotransferase

Query Match          50.68;   Score 44;   DB 2;   Length 192;
Best Local Similarity 62.58;   Pred. No. 30;
Matches     10;   Conservative      3;   Mismatches      3;   Indels      0;   Gaps      0;

OY      2    LYKFKKKLLKSLKRL 17
         | | | | | : | | |
Db       121  LSKTKRKQLKIIVKKL 136

Search completed: December 24, 2002, 09:20:06
Job time : 58 secs
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 24, 2002, 09:16:50 : Search time 11 seconds

(without alignments)  
67,870 Million cell updates/sec

Title: US-09-648-816b-3

Perfect score: 87

Sequence: 1 ALYKFKKKLLSLKRLG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	ID	Description
1	51	58.6	487 1	YD64_METUA
2	48	55.2	540 1	TOP1_AOUAE
3	45	51.7	90 1	PIF4_PIG
4	45	51.7	427 1	EBP2_YEAST
5	45	51.7	569 1	STY_TOBAC
6	44	50.6	192 1	KPY1_SPICT
7	44	50.6	243 1	CL12_HUMAN
8	44	50.6	828 1	YF44_YEAST
9	43.5	50.0	642 1	VR65_SCHPO
10	43	49.4	239 1	TRPA_THEMA
11	42	48.3	357 1	CKR9_HUMAN
12	42	48.3	369 1	CKR9_MOUSE
13	42	48.3	436 1	KP58_RAT
14	42	48.3	488 1	DHAL_BACST
15	42	48.3	704 1	GIGR_YEAST
16	42	48.3	1004 1	CARE_HUMAN
17	42	48.3	1165 1	STV_AOUAE
18	41	47.1	101 1	PLF4_HUMAN
19	41	47.1	105 1	PLF4_RAT
20	41	47.1	153 1	GLB2_ASCSU
21	41	47.1	221 1	MTE_BUCAI
22	41	47.1	488 1	DHAL_BACSU
23	41	47.1	520 1	CC3_YEAST
24	41	47.1	545 1	CMC1_YEAST
25	41	47.1	690 1	AFT1_YEAST
26	41	47.1	859 1	MUTS_AOUAE
27	41	47.1	1462 1	TOP2_PEA
28	40	46.0	149 1	YC13_ARCFU
29	40	46.0	158 1	MB27_BOVIN
30	40	46.0	171 1	CP18_BOVIN
31	40	46.0	172 1	TCTP_MOUSE
32	40	46.0	197 1	RP34_BPSPI
33	40	46.0	333 1	Y04P_BP74

34	40	46.0	340 1	VC47_HELPJ	O92jv0	helicobacte
35	40	46.0	340 1	VC47_HELPJ	O25842	helicobacte
36	40	46.0	359 1	AG25_HUMAN	Q13725	homo sapien
37	40	46.0	369 1	CNA1_YEAST	P22434	saccharomyc
38	40	46.0	413 1	RG82_HUMAN	P10264	homo sapien
39	40	46.0	425 1	RG82_MOUSE	O9CXP4	mus musculu
40	40	46.0	454 1	DNA4_BUCAP	P29434	buchnera ap
41	40	46.0	1076 1	PROB_ASTLO	P27059	astasia lon
42	40	46.0	1202 1	YE01_SCHPO	O13798	schizosacch
43	40	46.0	4427 1	PKSL_BACSU	O05470	bacillus su
44	40	44.8	54 1	STP1_MOUSE	P10856	mus musculu
45	39	44.8	85 1	PLF4_SHEEP	P30035	ovis aries

## ALIGNMENTS

```

RESULT 1
ID      YD64_METUA          STANDARD:      PRT:      487 AA.
AC      058759:
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein M01364.
GN      M01364.
OS      Methanococcus jannaschii.
OC      Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC      Methanocaldococcaceae; Methanocaldococcus.
OX      NCBI_TaxID=2190;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SRAIIN-JAL-1 / DSM 2661 / ATCC 43067;
RX      MEDLINE=96337999; PubMed=8688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA      Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA      Scott J.L., Geoghegan N.S.M., Meldrum J.F., Fuhmann J.L., Nguyen D.,
RA      Uutterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT      "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL      jannaschii."
RL      Science 273:1058-1073(1996).
CC      -1- SIMILARITY: BELONGS TO THE UPF0024 FAMILY.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC      EMBL: U67576; AAB99372.1; -
CC      TIGR: M01364; -
CC      InterPro: IPR001656: UPF0024.
CC      Pfam: PF01142: UPF0024; 1.
CC      PROSITE: PS01268; UPF0024; 1.
CC      Hypothetical protein; Complete proteome.
CC      SQUIDNCE 487 AA; 57426 MW; 1D8F68F634630604 CRC64;

```

```

Query Match      58.6%      Score 51; DB 1; Length 487;
Best Local Similarity 71.4%; Pred. No. 2;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY      3 YKRFKKLLSLKRLK 16
DB      264 YKRFKKLLSLKRLK 277

```

RESULT 2

TOP1\_AQUAE  
ID TOP1\_AQUAE STANDARD: PRT: 540 AA.  
AC 066893;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE DNA topoisomerase I (EC 5.99.1.2) (Omega protein) (Relaxing enzyme)  
DE (Unwinding enzyme) (Swivelase).  
GN TOPA OR AQ\_657.  
OS Bacteria; Aquificae; Aquificales; Aquificaceae;  
OC Aquifex aeolicus.  
OC Aquifex  
ON NCBI\_TaxID=63363;  
RX MEDLINE=98196666; PubMed=9537320;  
RC STRAIN=VF5;  
RP SEQUENCE FROM N.A.  
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,  
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,  
RT "The complete genome of the hyperthermophilic bacterium Aquifex  
aeolicus.";  
RL Nature 392:353-358(1998).  
CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE  
CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.  
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
DNA, followed by passage and rejoining.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA  
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN  
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS  
AT ONE END OF THE ENZYME-SEVERED DNA STRAND.  
CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE  
FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF000700; AAC06848.1; -.  
DR HSPD: P06612; 1ECL.  
DR InterPro: IPR002936; DNAPrim\_toprim.  
DR InterPro: IPR003601; DNATopi\_ATP\_bind.  
DR InterPro: IPR003602; DNATopi\_DNA\_bind.  
DR InterPro: IPR000380; Prok\_topisomase.  
DR Pfam: PF01131; Topoisom\_bac; 1.  
DR Pfam: PF01751; Toprim; 1.  
DR PRINTS: PRO0417; PRTPISMRASE1.  
DR SMART: SM00437; TOP1AC; 1.  
DR SMART: SM00436; TOP1BC; 1.  
DR SMART: SM00493; TOPRIM; 1.  
DR TIGRFAMs: TIGR01051; topa\_bact; 1.  
DR PROSITE: PS00396; TOPOISOMERASE\_I\_PROK; 1.  
DR Isomerase; Topoisomerase; DNA-binding; Complete proteome.  
FT ACT\_SITE 281 281 DNA CLEAVAGE (BY SIMILARITY).  
SQ SEQUENCE 540 AA; 63427 MW; 89C0604DF5B042E CRC64;  
Query Match 55.2%; Score 48; DB 1; Length 540;  
Best Local Similarity 56.2%; Pred. No. 6.2;  
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

AC P30034;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Platelet factor 4 (PF-4) (CXCL4).  
GN SCYB4 OR PF4.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
ON NCBI\_TaxID=9623;  
RX MEDLINE=9525268; PubMed=7737160;  
RC TISSUE=platelet;  
RP SEQUENCE, AND O-GLYCOSYLATION.  
RA Proudfoot A.E.I., Magrenat E., Haley T.M., Malone T.E., Wells T.N.C.;  
RT "The complete primary structure of glycosylated porcine platelet  
factor 4.";  
RL Eur. J. Biochem. 228:658-664(1995).  
RN [2]  
RP SEQUENCE OF 18-86.  
RC TISSUE=platelet;  
RX MEDLINE=92160127; PubMed=1788836;  
RA Shigeta O., Lu W., Holt J.C., Edmunds L.H. Jr., Niewiarowski S.;  
RT "Ovine platelet factor 4: purification, amino acid sequence,  
RT radioimmunoassay and comparison with platelet factor 4 of other  
RT species.";  
RL Thromb. Res. 64:509-520(1991).  
CC -1- FUNCTION: PLATELET FACTOR 4, NONCOVALENTLY BOUND TO A PROTEOGLYCAN  
MOLECULE, IS RELEASED DURING PLATELET AGGREGATION. PF4 NEUTRALIZES  
CC THE ANTICOAGULANT EFFECT OF HEPARIN BECAUSE IT BINDS MORE STRONGLY  
CC TO HEPARIN THAN TO THE CHONDROITIN-4-SULFATE CHAINS OF THE CARRIER  
CC MOLECULE. CHEMOTACTIC FOR NEUTROPHILS AND MONOCYTES.  
CC -1- SUBUNIT: HOMOTETRAMER.  
CC -1- PMW: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS  
CC MODIFIED WITH STALIC ACID RESIDUES (MICROHETEROGENETTY).  
CC -1- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXCL).  
DR HSPD: P02777; 1PLF.  
DR InterPro: IPR001089; CXCL\_chmkine-smll.  
DR InterPro: IPR001811; Chemokine\_il8.  
DR Pfam: PF00048; Il8; 1.  
DR PRINTS: PR00437; SMALCYTKCXC.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW Cytokine; Platelet; Heparin-binding; Chemotaxis; Glycoprotein.  
FT MOD\_RES 1 8 O-LINKED (GALNAC. . .).  
FT CAROYHD 25 51 BY SIMILARITY.  
FT DISULFD 27 67 BY SIMILARITY.  
FT DISULFD 43 43 E -> I (IN REF. 2).  
FT CONFLICT 85 86 SO -> PE (IN REF. 2).  
FT CONFLICT 85 86  
SQ SEQUENCE 90 AA; 9644 MW; 108F15AC828FDB6F CRC64;  
Query Match 51.7%; Score 45; DB 1; Length 90;  
Best Local Similarity 83.3%; Pred. No. 3;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4  
EBP2\_YEAST  
ID EBP2\_YEAST STANDARD: PRT: 427 AA.  
AC P36049;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE rRNA processing protein EBP2 (EBNA1-binding protein homolog).  
GN EBP2 OR YKL172W OR YKL636.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

```

OC Saccharomycetales: Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288c;
RX MEDLINE=94378719; PubMed=8091858;
RA vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger F.;
RT "Sequencing and analysis of a 20.5 kb DNA segment located on the left
RL arm of yeast chromosome XI.";
RN Yeast 10:S25-S33(1994).
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX PubMed=10947841;
RA Tsuji R., Miyoshi K., Tsuno A., Matsui Y., Toh-e A., Miyakawa T.,
RA Mizuta K.;
RT "Ebp2p, yeast homologue of a human protein that interacts with
RT Epstein-Barr virus nuclear antigen 1, is required for pre-rRNA
RT processing and ribosomal subunit assembly.";
RL Genes Cells 5:543-553(2000).
RN [3]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX PubMed=10849420;
RA Huber M.D., Doreet J.H., Shire K., Frappier L., McLearn M.A.;
RT "The budding yeast homolog of the human EBNA1-binding protein 2
RT (Ebp2p) is an essential nuclear protein required for pre-rRNA
RT processing.";
RL J. Biol. Chem. 275:28764-28773(2000).
CC -1- FUNCTION: Required for the processing of the 27S pre-rRNA.
CC -1- Probably involved in the step of the processing of the 27 SA
CC precursor into the 27 SB intermediate.
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -1- SIMILARITY: BELONGS TO THE EBP2 FAMILY.
CC
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CC -----
DR EMBL: Z26878; CAA81515.1; -
DR EMBL: Z28172; CAA82014.1; -
DR PIR: S38002; S38002.
DR PIR: S38409; S38409.
DR PIR: S44589; S44589.
DR SGD: S0001655; EBP2.
KW Ribosome biogenesis; Nuclear protein; Coiled coil.
FT DOMAIN 45 174 COILED COIL (POTENTIAL).
FT DOMAIN 234 265 COILED COIL (POTENTIAL).
FT DOMAIN 281 348 COILED COIL (POTENTIAL).
SQ SEQUENCE 427 AA: 49734 MW: 44116 CDF79DB5A CRC64;
Query Match 51.7%; Score 45; DB 1; Length 427;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ALYKFKKKLKSLKRL 17
DB 75 ALSKKEKKRLKKELKKM 91
RESULT 5
AC Q43794;
AC STRAIN=5288c;
AC STANDARD; PRT; 569 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (GluRS).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spectromorphia; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. SR1; TISSUE=leaf;
RA Andersen R.V.;
RT Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: X83524; CAA58506.1; -
DR HSSP: P27000; IGLN.
DR InterPro: IPR004527; GluX_bact.
DR InterPro: IPR000924; Glu tRNA-synt_1c.
DR InterPro: IPR001412; tRNA-synt_1.
DR Pfam: PF00748; tRNA-synt_1c; 1.
DR PRINTS: PR00987; TRNASYNTGLU.
DR TIGRFAMs: TIGR00464; gltX_bact; 1.
DR PROSITE: PS00178; AA-tRNA-LIGASE_1; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE 62 72 "HIGH" REGION.
FT SITE 303 307 "KMSK" REGION.
FT BINDING 306 306 ATP (BY SIMILARITY).
SQ SEQUENCE 569 AA: 63338 MW: F2E81D73460A1844 CRC64;
Query Match 51.7%; Score 45; DB 1; Length 569;
Best Local Similarity 69.2%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKKKLKLS 13
DB 141 ALYKFAFKELQS 153
RESULT 6
AC KPYL_SPLIC
ID KPYL_SPLIC STANDARD; PRT; 192 AA.
AC P19680; O30600;
DT 01-FEB-1991 (Rel. 17, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyruvate kinase (EC 2.7.1.40) (PK) (Fragment).
CN PYK.
OS Spiroplasma citri.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_TaxID=2133;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27556 / R8A2;
RX MEDLINE=90236934; PubMed=2139649;
RA Chevalier C., Sallard C., Bove J.M.;
RT "Organization and nucleotide sequences of the Spiroplasma citri genes
RT for ribosomal protein S2, elongation factor Ts, spiralin,
RT phosphofructokinase, pyruvate kinase, and an unidentified protein.";
RL J. Bacteriol. 172:2693-2703(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Le Dantec L.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
CC -1- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.
CC -1- PATHWAY: Glycolysis; final step.

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CC -1- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: AF012877; AAB69999.1; -.
CC
CC PIR: F35270; F35270.
CC
CC HSSP: P14178; 1PKY.
CC InterPro: IPR001697; Pyruvate_kinase.
CC Pfam: PF00224; PK; 1.
CC Prodom: PD001009; Pyruvate_kinase; 1.
CC Prosite: PS00110; PYRUVATE_KINASE; PARTIAL.
CC Transferase: kinase; Glycolysis; Multigene family; Magnesium.
CC CONFLICT 82 192 HRRIGLOKSNITVYHOMNNSIMFSPCKFLHYHTLLS
CC KTKKOLKIVKRLKLOSOHNLAHGLRETTSSCFNRR
CC PSIMRLSEFOIVTSFKISLVKLIK -> RAGIKKG
CC KOEIVAGATVITVSLPTQNEGTGTEITVSYDSOLKV
CC GGVVLVDDGKIQIANTVGIKPIIETKA (IN REF. 2).
CC
CC NON_TER 192 192 ACF22444BF2CF807 CRC64;
CC SEQUENCE 192 AA; 22209 MW;
CC
CC Query Match 50.6%; Score 44; DB 1; Length 192;
CC Best Local Similarity 62.5%; Pred. No. 9;
CC Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
CC
QY 2 LYKKFKKLLKSLRL 17
DB 121 LSKTKKOLKIVKRL 136

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CC RESULT 7
CC CL12_HUMAN
CC ID CL12_HUMAN STANDARD; PRT; 243 AA.
CC AC 015247; O15174;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Chloride intracellular channel protein 2 (XAP121).
CC GN CLIC2
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC OX NCBI_Taxid=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=97480736; PubMed=9339381;
CC RA Helms N.S., Pousetka A.;
CC RT "Genomic structure of a novel chloride channel gene, CLIC2, in Xq28.";
CC RL Genomics 45:224-228(1997).
CC -1- FUNCTION: Possible chloride ion channel.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL LIVER AND ADULT SKELETAL
CC MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE CLIC FAMILY OF CHLORIDE CHANNELS.
CC -----
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CC -----
CC EMBL: Y12696; CAA73228.1; -.
CC EMBL: AJ000217; CAA03948.1; -.
CC EMBL: AJ000218; CAA03948.1; JOINED.
CC EMBL: AJ000219; CAA03948.1; JOINED.
CC Genew: HGNC:2063; CLIC2.
CC MIM: 300138; -.

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DR InterPro: IPR002946; Int.Cl_channel.
DR PRINTS: PRO1263; INTCLCHANNEL.
DR TIGRfams: TIGR00862; O-CLC; 1.
CC KW Ionic channel; Ion transport; Voltage-gated channel.
CC CONFLICT 109 109 S -> C (IN REF. 1; CAA03948).
CC FT CONFLICT 164 164 G -> E (IN REF. 1; CAA03948).
CC FT CONFLICT 164 164
CC SEQUENCE 243 AA; 27812 MW; 7887E05DF27EF73 CRC64;
CC
CC Query Match 50.6%; Score 44; DB 1; Length 243;
CC Best Local Similarity 64.38; Pred. No. 11;
CC Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC
QY 4 KFKKKLLKSLRL 17
DB 133 KNFKSLKKEPKRL 146

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CC RESULT 8
CC YFA4_YEAST
CC ID YFA4_YEAST STANDARD; PRT; 828 AA.
CC AC P43585;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Hypothetical 95.4 kDa protein in SEC4-MSH4 intergenic region.
CC YF1004W.
CC OS Saccharomyces cerevisiae (Baker's yeast).
CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CC OX NCBI_Taxid=4932;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=S288c / AB972;
CC RX MEDLINE=95400292; PubMed=7670463;
CC RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
CC Sasayama S.-I., Sasayama M., Tsuchiya Y., Soeda E., Yokoyama K.,
CC Yamazaki M., Tashiro H., Eki T.;
CC RT "Analysis of the nucleotide sequence of chromosome VI from
CC Saccharomyces cerevisiae.";
CC RL Nat. Genet. 10:261-268(1995).
CC
CC [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=S288c / AB972;
CC RX MEDLINE=96381249; PubMed=8789262;
CC RA Naitou M., Ozawa M., Sasayama S.-I., Kobayashi M., Hagiwara H.,
CC Shibata T., Hanaoka F., Watanabe K., Ono A., Yamazaki M., Tashiro H.,
CC Eki T., Murakami Y.;
CC RT "Sequencing of a 23 kb fragment from Saccharomyces cerevisiae
CC chromosome VI.";
CC RL Yeast 12:77-84(1996).
CC -1- SIMILARITY: TO YEAST YJL012C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D50617; BAA09234.1; -.
CC DR SGD: S0001890; PHML.
CC DR InterPro: IPR00431; SPX.
CC DR Pfam: PF03105; SPX; 1.
CC KW Hypothetical protein; Transmembrane.
CC FT TRANSMEM 728 748 POTENTIAL.
CC FT TRANSMEM 767 787
CC SEQUENCE 828 AA; 95440 MW; BCEF34FDB2012ABD CRC64;
CC
CC Query Match 50.6%; Score 44; DB 1; Length 828;
CC Best Local Similarity 60.0%; Pred. No. 38;
CC Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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OY 4 KKKKKLLSKLR 18  
 DB 357 KKKKKLLSKLR 371

RESULT 9  
 YB65\_SCHPO STANDARD: PRI: 642 AA.  
 AC 009746:  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE Hypothetical protein C12C2.05c in chromosome II.  
 GN SPBC12C2.05c.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 NX NCBI\_TaxID=4896;  
 RN 11

SEQUENCE FROM N.A.  
 RP STRAIN=972:  
 RX MEDLINE=21849401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.D., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver P., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Stevens S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnietz B.,  
 RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Punelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.,  
 RT "The genome sequence of Schizosaccharomyces pombe."  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 BINDING DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 FCH DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
 CC -1- SIMILARITY: TO YEAST BZ1.  
 CC -----  
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 CC -----  
 CC EMBL: 254140; CAA90818.1;  
 DR HSSP: P29354; 1GFC.  
 DR InterPro: IPR001060; Cdc15\_Fes\_CTP4.  
 DR InterPro: IPR002219; DAG\_PE-bind.  
 DR InterPro: IPR001452; SH3.  
 DR Pfam: PF00018; SH3; 2.  
 DR Pfam: PF00130; DAG\_PE-bind; 1.  
 DR Pfam: PF00611; FCH; 1.  
 DR PRINTS: PR00008; DAGPEOMAIN.  
 DR ProDom: PD000066; SH3; 2.

DR SMART: SM00109; C1; 1.  
 DR SMART: SM00055; FCH; 1.  
 DR SMART: SM00326; SH3; 2.  
 DR PROSITE: PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE: PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE: PS50133; FCH; 1.  
 DR PROSITE: PS50002; SH3; 2.  
 KW Hypothetical protein; SH3 domain; Zinc; Phorbol-ester binding; Repeat;  
 KW Coiled coil.  
 FT DOMAIN 6 FCH.  
 FT DOMAIN 113 190 COILED COIL (POTENTIAL).  
 FT DOMAIN 397 447 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 521 575 SH3 1.  
 FT DOMAIN 584 642 SH3 2.  
 SO SEQUENCE 642 AA: 72216 MW: E6770ED15BD73D3C CRC64;  
 Query Match 50.0%; Score 43.5; DB 1; Length 642;  
 Best Local Similarity 61.1%; Pred. No. 35;  
 Matches 11; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

OY 2 LYKFF---KKKLLSKLR 16  
 DB 136 LYKFFSSEKETLNSYKR 153

RESULT 10  
 TRPA\_THEMA STANDARD: PRI: 239 AA.  
 ID TRPA\_THEMA  
 AC P50908;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tryptophan synthase alpha chain (EC 4.2.1.20).  
 DE TRPA OR TM0137.  
 CN Thermotoga maritima.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales;  
 OC Thermotogaceae; Thermotoga.  
 NX NCBI\_TaxID=2336;  
 RN 11

SEQUENCE FROM N.A.  
 RP MEDLINE=96003619; PubMed=7556082;  
 RX Steiner R., Dahm A., Darimont B., Ivens A., Liedl W., Kirschner K.,  
 RA "Beta alpha(8)-barrel proteins of tryptophan biosynthesis in the  
 RT hyperthermophile Thermotoga maritima."  
 RL EMBO J. 14:4395-4402(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB / DSM 3109;  
 RX MEDLINE=99287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of Thermotoga maritima."  
 RL Nature 399:323-329(1999).  
 CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE  
 CC OF INDOLEGLYCEROL PHOSPHATE TO INDOLE AND GLYCERALDEHYDE 3-  
 CC PHOSPHATE.  
 CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate  
 CC = L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.  
 CC -1- PATHWAY: tryptophan biosynthesis; fifth (last) step.  
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (by  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.  
 CC -----  
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CC
DR      EMBL: A1133336; CAB43480.1; -
DR      EMBL: A1131357; CAB66136.2; -
DR      MGD: MGI:1341902; Cmkbr10.
DR      InterPro: IPR004069; CC_chemkineg.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PRINTS: PR01531; CHEMOKINER9.
DR      PRINTS: PR00237; GPCR_RHODPSN.
DR      PROSITE: PS00237; G_PROTEIN_RECIP_F1.1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECIP_F1.2; 1.
DR      KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
KW      DOMAIN 1
KW      TRANSMEM 50 76
KW      FT      TRANSMEM 77 85
KW      FT      TRANSMEM 86 106
KW      FT      DOMAIN 107 120
KW      FT      TRANSMEM 121 142
KW      FT      DOMAIN 143 160
KW      FT      TRANSMEM 161 181
KW      FT      TRANSMEM 182 210
KW      FT      TRANSMEM 211 238
KW      FT      DOMAIN 239 254
KW      FT      TRANSMEM 255 280
KW      FT      DOMAIN 281 304
KW      FT      TRANSMEM 305 322
KW      FT      DOMAIN 323 369
KW      FT      CARBOHYD 32 32
KW      FT      DISULFID 119 198
KW      SQ      SEQUENCE 369 AA; 41913 MW; 6971f76f0a24b4ae cnc64;
OY      4 KKKKKLLKSLKRLG 18
DB      322 ERFRLDVLKTKNLG 336
OY      :::::|::|::|
DB      322 ERFRLDVLKTKNLG 336
RESULT 13
ID      KP58_RAT
AC      P46892;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Galactosyltransferase associated protein kinase p58/GTA (EC 2.7.1.-).
DE      CDC2L1.
OS      Rattus norvegicus (Rat).
CN      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Sprague-Dawley; TISSUE=Salivary gland;
RX      MEDLINE=94325346; PubMed=8049264;
RA      Kerr M., Fischer J.E., Purushotham K.R., Gao D., Nakagawa Y.,
RA      Maeda N., Ghanta V., Hiramoto R., Chegini N., Humphreys-Beher M.G.;
RT      "Characterization of and the synthesis and expression of the GTA-kinase
RT      from transformed and normal rodent cells.";
RL      Biochim. Biophys. Acta 1218:375-387(1994).
CC      -!- FUNCTION: ACTS AS A NEGATIVE REGULATOR OF THE NORMAL CELL CYCLE
CC      PROGRESSION. IN VITRO, THIS PROTEIN KINASE HAS BEEN SHOWN TO
CC      PHOSPHORYLATE A NUMBER OF SUBSTRATES, INCLUDING HISTONE H1,

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CC CASEIN, AND GALACTOSYLTRANSFERASE. MAY FUNCTION IN REGULATING
CC PROLIFERATION BY THE PHOSPHORYLATION AND SUBSEQUENT PLASMA
CC MEMBRANE TARGETING OF GALACTOSYLTRANSFERASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC, NUCLEAR AND PERINUCLEAR
CC MEMBRANES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CCKX SUBFAMILY.
CC -----
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CC -----
DR EMBL: L24388; AAA89509.1; ALT_INIT.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase: 1.
DR ProDom: PD000001; Euk_pkinase: 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle.
FT DOMAIN 25 30 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 30 44 CALMODULIN-BINDING (POTENTIAL).
FT FT NP_BIND 79 364 PROTEIN KINASE.
FT BINDING 85 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 203 203 BY SIMILARITY.
SQ SEQUENCE 436 AA; 49547 MW; D2BA9BC73EAD3D27 CRC64;

Query Match 48.3%; Score 42; DB 1; Length 436;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 KKKFKLLKSLKRLG 18
   ||::||:| | | |
Db 26 KKKRKKLVKGLHRA 40

RESULT 14
ID DHAL_BACST STANDARD; PRT; 488 AA.
AC P42329;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase, thermostable (PC 1.2.1.3).
DE ADHMT.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLC1;
RA Imanaka T., Ohta T., Sakoda H., Widyastuti N., Matsunaka M.;
RT "Cloning, nucleotide sequence, and efficient expression of the gene
RT coding for thermostable aldehyde dehydrogenase from Bacillus
RT stearothermophilus, and characterization of the enzyme.";
RL J. ferment. Bieng. 76:161-167(1993).
CC -1- FUNCTION: OXIDIZES SEVERAL ALIPHATIC ALDEHYDES, PARTICULARLY C6-
CC ALIPHATIC ALDEHYDE AND HEXANAL, BUT DO NOT OXIDIZE BENZALDEHYDE.
CC THE OPTIMUM TEMPERATURE IS AROUND 55 AND 60 DEGREES CELSIUS.
CC -1- CATALYTIC ACTIVITY: an aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- COFACTOR: REQUIRES EITHER NAD OR NADP AS A COENZYM.
CC -1- PATHWAY: Ethanol utilization; second step.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC -----

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DR EMBL: D13846; BAA02975.1; -  
 DR HSSP: P51977; IBXS.  
 DR InterPro: IPR002086; Aldenhyde\_dehydr.  
 DR Pfam: PF00171; aldedh. 1.  
 DR PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS. 1.  
 DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU. 1.  
 KW Oxidoreductase; NAD.  
 FT NP\_BIND 233 238 NAD (ADP PART) (BY SIMILARITY).  
 FT ACT\_SITE 255 255 BY SIMILARITY.  
 FT ACT\_SITE 289 289 BY SIMILARITY.  
 SQ SEQUENCE 488 AA; 52915 MW; 29B824451985D5DED CRC64;

Query Match 48.3%; Score 42; DB 1; Length 488;  
 Best Local Similarity 50.0%; Pred. No. 45;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 LYKFKKKLKSLKRL 17  
 DB 301 YVEPFKALLERVKOL 316

RESULT 15  
 GLOB\_YEAST  
 ID GLOB\_YEAST STANDARD; PRT; 704 AA.  
 AC P32775;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching  
 DE enzyme)  
 GN GLC3 OR YEL011W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_Taxid=4932;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=92340576; PubMed=1634552.  
 RX Thon V.J., Vigneron-Lesens C., Marianne-Pepin T., Montreuil J.,  
 RA Decq A., Rachez C., Ball S.G., Cannon J.F.;  
 RT "Coordinate regulation of glycogen metabolism in the yeast  
 RT Saccharomyces cerevisiae. Induction of glycogen branching enzyme.";  
 RL J. Biol. Chem. 267:15224-15228(1992).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=5288c / AB972;  
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,  
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,  
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,  
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Mosedale D., Nakahara K., Namath A., Norgren R., Oelher P., Oh C.,  
 RA Petrel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,  
 RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of  
 CC glycogen.  
 CC -1- PATHWAY: Glycogen biosynthesis; third step.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE  
 CC LATE EXPONENTIAL AND STATIONARY GROWTH PHASES, COINCIDENT WITH  
 CC MAXIMAL GLYCOGEN ACCUMULATION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M76739; AAA34632.1; -  
 DR EMBL: U18530; AAB64488.1; -  
 DR PIR: A42752; A42752.  
 DR SGD: S0000737; GLC3.  
 DR InterPro: IPR00461; Alpha-amylase.  
 DR InterPro: IPR004193; Isoamylase\_N.  
 DR Pfam: PF00128; alpha-amylase. 1.  
 DR Pfam: PF02922; Isoamylase\_N. 1.  
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase.  
 FT ACT\_SITE 356 356 BY SIMILARITY.  
 FT ACT\_SITE 417 417 BY SIMILARITY.  
 FT ACT\_SITE 486 486 BY SIMILARITY.  
 FT CONFLICT 564 564 S -> T (IN REF. 1).  
 SQ SEQUENCE 704 AA; 81115 MW; 9C227E107B825F27 CRC64;

Query Match 48.3%; Score 42; DB 1; Length 704;  
 Best Local Similarity 50.0%; Pred. No. 65;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 YKFKKKLKSLKRLG 18  
 DB 213 YKFKTEKVLPRIKVLG 228

Search completed: December 24, 2002, 09:18:46  
 Job time : 14 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

```
Run on:      December 24, 2002, 09:16:51 ; Search time 29 Seconds
              (without alignments)
              127.891 Million cell updates/sec
```

Title: US-09-648-816B-3  
Page: 87

Sequence: 1 ALYKKFKKLLKSLKRLG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database

```

1:  SPtrembl_21.*
2:  sp.bacteria.*
3:  sp.fungi.*
4:  sp.human.*
5:  sp.invertebrate.*
6:  sp.mammal.*
7:  sp.mmc.*
8:  sp.organelle.*
9:  sp.phage.*
10: sp.plant.*
11: sp.podent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	47	54.0	139	17	Q9V132	Q9V132 pyrococcus
2	46	52.9	215	2	Q9Z655	Q9Z655 zymomonas m
3	46	52.9	399	5	Q25166	Q25166 spirochaeta m
4	46	52.9	472	10	Q98R07	Q98R07 quillardia
5	46	52.9	741	3	Q9P5P3	Q9P5P3 neurospora
6	45	51.7	75	16	Q99Z45	Q99Z45 streptococcus
7	45	51.7	140	17	Q59212	Q59212 pyrococcus
8	45	51.7	160	5	Q9TPP3	Q9TPP3 caenorhabdi
9	45	51.7	187	16	Q9ZEX3	Q9ZEX3 listeria in
10	45	51.7	248	11	Q9D423	Q9D423 mus musculus
11	45	51.7	568	11	Q54955	Q54955 mus musculus
12	45	51.7	568	11	Q8ROX7	Q8ROX7 mus musculus
13	45	51.7	4146	13	Q9DEI1	Q9DEI1 xenopus lae
14	45	51.7	6885	4	Q8KXK0	Q8KXK0 homo sapien
15	44.5	51.1	615	10	Q9L0D9	Q9L0D9 arabidopsis
16	44	50.6	246	16	Q8RAL7	Q8RAL7 thermotoga

17	44	50.6	247	4	08RCE3	08tce3 homo sapien
18	44	50.6	254	8	09BRW7	09brw7 guillardia
19	44	50.6	266	17	097YL4	097yl4 sulfolobus
20	44	50.6	437	12	09OAH9	09gah9 murid herpe
21	44	50.6	460	12	041969	041969 murid herpe
22	44	50.6	511	5	08WTL1	08wtl1 caenorhabdi
23	44	50.6	531	5	095X11	095x11 caenorhabdi
24	44	50.6	729	3	074985	074985 schizosacch
25	44	50.6	778	12	084509	084509 paramecium
26	44	50.6	841	2	09AIP3	09aip3 carsonella
27	43.5	50.0	69	17	08RTX3	08rtx3 methanopyru
28	43	49.4	139	17	08ZVC7	08zvc7 pyrobaculum
29	43	49.4	398	5	002339	002339 caenorhabdi
30	43	49.4	439	2	053589	053589 staphylococ
31	43	49.4	460	17	096Y49	096y49 sulfolobus
32	43	49.4	477	16	08R6Z4	08r6z4 thermoaerob
33	43	49.4	497	16	09G9R3	09gr73 staphylococ
34	43	49.4	727	16	08YZG7	08yzg7 arabidopsi
35	42.5	48.9	141	12	09YW61	09yw61 melanopus
36	42	48.3	145	2	09AHM6	09ahm6 carsonella
37	42	48.3	175	16	08XND4	08xnd4 clostridium
38	42	48.3	318	16	08RFB0	08rfb0 fribacterium
39	42	48.3	369	4	09UO06	09uog6 homo sapien
40	42	48.3	420	11	099LT9	099lt9 mus musculus
41	42	48.3	427	2	P97242	P97242 helicobacte
42	42	48.3	427	2	088126	088126 helicobacte
43	42	48.3	427	16	034491	034491 helicobacte
44	42	48.3	427	16	034945	034945 helicobacte
45	42	48.3	558	10	Q9M175	Q9m175 arabidopsi

## ALIGNMENTS

ID	Q9V132	PRELIMINARY:	PRT:	139 AA.
AC	Q9V132:			
DT	01-MAY-2000 (TREMblrel, 13, Created)			
DT	01-MAY-2000 (TREMblrel, 13, Last sequence update)			
DT	01-JUN-2002 (TREMblrel, 21, Last annotation update)			
DE	Hypoetical protein PAB2A13.			
GN	PAB2A13.			
OS	Pyrococcus abyssi.			
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;			
OC	Pyrococcus.			
OX	NCBI_TaxID=29292;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ORSAY;			
RA	Heilig R.;			
RT	"Pyrococcus abyssi genome sequence: insights into archaeal chromosomes			
RT	structure and evolution."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, AJ248284, CAB49519.1;			
DR	InterPro: IPR000637; AT_hoek; 1.			
DR	Pfam: PF02178; AT_hoek; 1.			
DR	SMART: SM00384; AT_hoek; 1.			
DR	TIGRFAMS: TIGR01199; HTH_fis; 1.			
KM	Hypoetical protein: Complete proteome.			
SO	SEQUENCE 139 AA; 16215 MW; 5B72C93C2398A060 CRC64;			

Query Match	54.08;	Score 47;	DB 17;	Length 139;
Best Local Similarity	44.48;	Pred. No. 23;		
Matches	8;	Conservative	7;	Mismatches 3;
			Indels	0;
			Gaps	0

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QY      1 ADYKKKFKKKLLKSLKRLG 18
        :11 | 11::1::1
Db      60 SLYPKVSKVLRALEQMG 77

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AC 099245;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Hypothetical protein SPY1405.  
 GN SPY1405.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / SPROTYPE M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 DR EMBL: AE006577; AAK34220.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 75 AA: 8716 MW: 49A8B063A7E91BC CRC64;

Query Match  
 Best Local Similarity 51.7%; Score 45; DB 16; Length 75;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 LYKFKKKLKLKRL 17  
 52 LEKFKNRRLKLNKRL 67

RESULT 7  
 ID 059212 PRELIMINARY; PRT; 140 AA.  
 AC 059212;  
 DT 01-AUG-1998 (TReMBLrel. 07, Created)  
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Hypothetical protein PH1560.  
 GN PH1560.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=96344137; PubMed=9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3."  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL: AP000006; BAA30672.1; -  
 DR InterPro: IPR000637; AT-hook.  
 DR Pfam: PF02178; AT-hook\_1.  
 DR SMART: SM00384; AT-hook\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 140 AA: 16271 MW: 53E3820315634968 CRC64;

Query Match  
 Best Local Similarity 51.7%; Score 45; DB 17; Length 140;  
 Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ALYKFKKKLKLKRLG 18  
 60 SLYKFKKKVMALEOMG 77

RESULT 8  
 ID 09793 PRELIMINARY; PRT; 160 AA.  
 AC 09793;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE H14E04.4 protein.  
 GN H14E04.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabdilita; Rhabdiloidea;  
 OC Rhabdilitidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans."  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Becker M., Wamsley P., Twyman B., Beck C., Bradshaw H.;  
 RT "The sequence of C. elegans cosmid H14E04."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF125448; AAD12811.1; -  
 SQ SEQUENCE 160 AA: 18294 MW: 5CEE2BC08F7043C CRC64;

Query Match  
 Best Local Similarity 51.7%; Score 45; DB 5; Length 160;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 3 YKFKKKLKLKRLG 18  
 111 FQNSKKFLKLNKRF 126

RESULT 9  
 ID 092EK3 PRELIMINARY; PRT; 187 AA.  
 AC 092EK3;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Hypothetical protein lin0456.  
 GN lin0456.  
 OS Listeria innocua.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Listeriaceae; Listeria.  
 OX NCBI\_TaxID=1642;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CLIP 11262 / SPROVAR 6A;  
 RX PubMed=11679669;  
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bioecker H., Brandt P., Chakraborty T.,  
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Delhoux P.,  
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
 RA Ettian K.-D., Fsihi B., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,  
 RA Jones L.-M., Kaerst U., Kreft J., Kunz M., Kunst F., Kurapat G.,  
 RA Madueno E., Maitournan A., Mata Vicente J., Ng E., Nedjari H.,  
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
 RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,  
 RT "Comparative genomics of *Listeria* species.",  
 RL Science 294:849-852(2001).  
 DR EMBL: AL596165; CAC95688.1; -  
 DR Listlist: LIND00456; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 187 AA; 22550 MW; F0182AE73143F2A0 CRC64;

Query Match 51.7%; Score 45; DB 16; Length 187;  
 Best Local Similarity 46.7%; Pred. No. 57;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 2 LYKRRKKLKLKSLKRL 16  
 Db 171 LYKRRKKLKLKSLKRL 185

RESULT 10  
 Q9D423 ID Q9D423 PRELIMINARY; PRT; 248 AA.  
 AC Q9D423;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE 4933421B21R1K protein.  
 GN 4933421B21R1K.  
 OS Mus musculus (Mouse).  
 OC Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 OX 11;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=TESTIS;  
 RC MEDLINE=21085660; Pubmed=11217851;  
 RX Medline=21085660; Pubmed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Knudl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK016857; BAB30468.1; -  
 DR MGD: MGI:1918324; 4933421B21R1K.  
 SQ SEQUENCE 248 AA; 29130 MW; FAF610B0EB2654D CRC64;

Query Match 51.7%; Score 45; DB 11; Length 248;  
 Best Local Similarity 47.1%; Pred. No. 74;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 2 LYKRRKKLKLKSLKRLG 18  
 Db 11 LYKRRKKLKLKSLKRLG 18

Db 57 LYHRYRKCISERRKRLG 73

RESULT 11  
 AC 054955 PRELIMINARY; PRT; 568 AA.  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).  
 GN SGP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 OX 11;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J;  
 RC MEDLINE=98125521; Pubmed=9464245;  
 RX Zhou J., Saba J.D.,  
 RA "Identification of the first mammalian sphingosine phosphate lyase  
 RT gene and its functional expression in yeast.",  
 RL Biochem. Biophys. Res. Commun. 242:502-507(1998).  
 CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (UDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL: AF036894; AAC03768.1; -  
 DR MGD: MGI:1261415; Sgp11.  
 DR InterPro: IPR002129; Pyridoxal\_dec.  
 DR Pfam: PF00282; Pyridoxal\_dec; 1.  
 KW Decarboxylase; Lyase; Pyridoxal phosphate.  
 SQ SEQUENCE 568 AA; 63707 MW; BA1852FE42D0F09 CRC64;

Query Match 51.7%; Score 45; DB 11; Length 568;  
 Best Local Similarity 41.2%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ALYKRRKKLKLKSLKRL 17  
 Db 65 SLMSRRKKLFLKRLKRM 81

RESULT 12  
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 AC Q8ROX7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Sphingosine phosphate lyase 1.  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 OX 11;  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=LIVER;  
 RC Straussberg R.;  
 RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC026135; AAH26135.1; -  
 KW Lyase.  
 SQ SEQUENCE 568 AA; 63677 MW; FAF5D2E4E49DF09E CRC64;

Query Match 51.7%; Score 45; DB 11; Length 568;  
 Best Local Similarity 41.2%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ALYKRRKKLKLKSLKRL 17  
 Db 65 SLMSRRKKLFLKRLKRM 81

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DR PROSITE: PS00019: ACTININ.1; UNKNOWN.1.
DR PROSITE: PS00402: BPD_TRANSF_INN_MEMBER; UNKNOWN.1.
DR PROSITE: PS50021: CH.2.
SQ SEQUENCE 6885 AA: 796205 MW: C778BE957A443398 CRC64;

Query Match          51.1%; Score 45; DB 4; Length 6885;
Best Local Similarity 52.2%; Pred. No. 1.4e+03;
Matches 12; Conservative 1; Mismatches 4; Indels 6; Gaps 1

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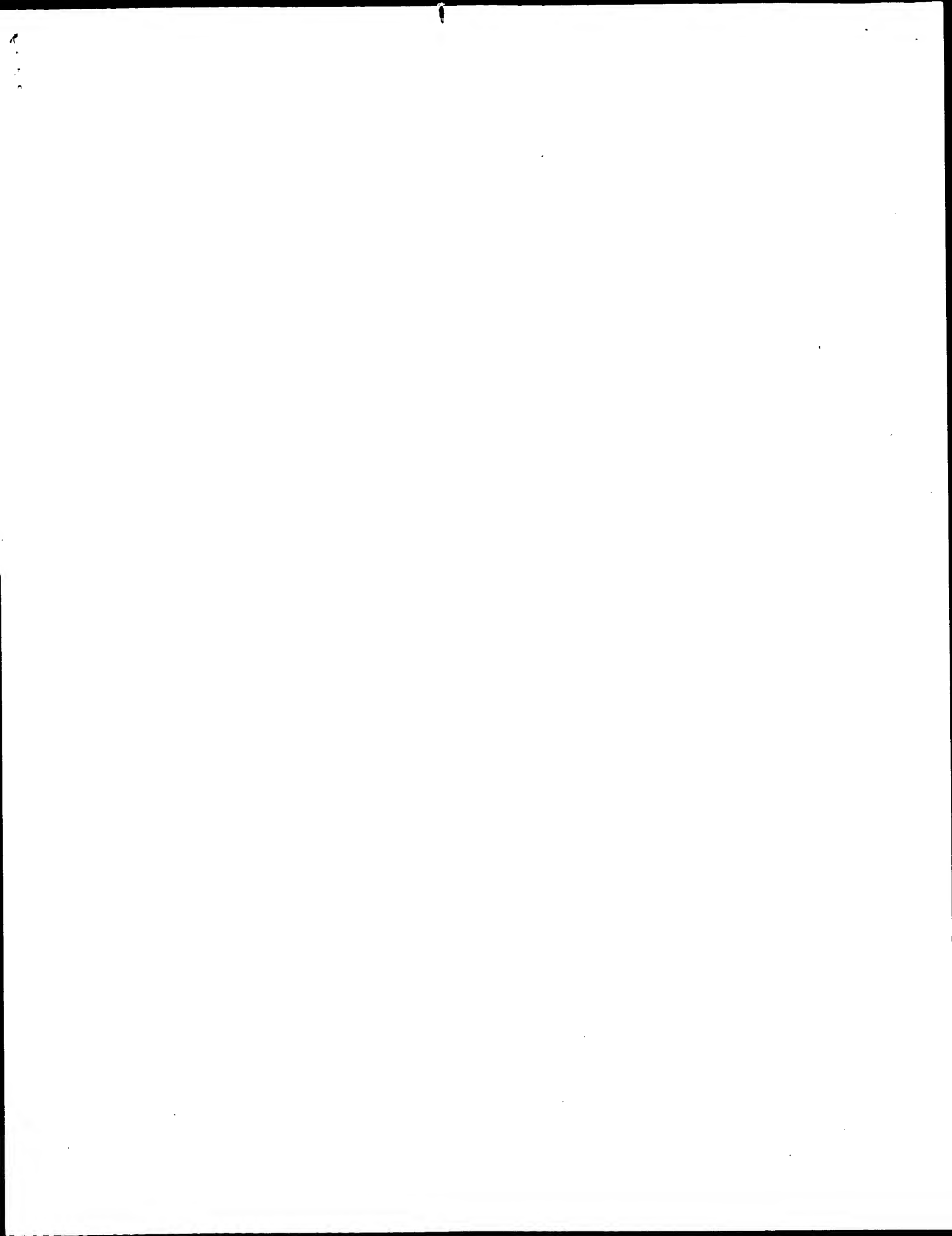
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AC O9LOP9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F24B9.17 protein.
GN F24B9.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P.,
RA Toriumi M., Chin C., Choi E., Chou J., Gonzalez A., Chung M.,
RA Hong B., Koo T., Li J., Liu A., Vayberg M., Alrafi H., Brooks S.,
RA Biehler E., Chao Q., Conn L., Conway A.B., Hansen N.,
RA Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C.,
RA Shin P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007583; AAF75081.1; -
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR004140; Exo70.
DR Pfam: PF03081; Exo70.1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN.1.
SQ SEQUENCE 615 AA: 68401 MW: 02CAEBBE04448622 CRC64;

Query Match          51.1%; Score 44.5; DB 10; Length 615;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 1; Gaps 1.

QY 2 LYKFKKKLL-KSLKRLG 18
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Db 199 IYKFKRKIIYDTLSHLG 216

Search completed: December 24, 2002, 09:20:43
Job time : 33 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2002, 09:16:50 ; Search time 10 seconds  
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30.174 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87

Sequence: 1 ALYKFKKKLKLKLRUG 18

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCIT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	46	52.9	46	US-10-036-869-11	Sequence 11, Appl
2	43	49.4	439	US-09-815-242-5696	Sequence 5696, Appl
3	42	48.3	108	US-09-822-263-14	Sequence 14, Appl
4	42	48.3	357	US-09-903-377-2	Sequence 2, Appl
5	42	48.3	357	US-09-952-385-2	Sequence 2, Appl
6	42	48.3	357	US-10-000-759A-2	Sequence 2, Appl
7	42	48.3	1004	US-09-767-215-2	Sequence 2, Appl
8	42	48.3	1138	US-09-767-215-2	Sequence 2, Appl
9	41	47.1	13	US-09-765-614B-31	Sequence 31, Appl
10	41	47.1	13	US-09-925-715-27	Sequence 27, Appl
11	41	47.1	13	US-10-036-869-9	Sequence 9, Appl
12	41	47.1	70	US-09-792-793A-91	Sequence 91, Appl
13	41	47.1	70	US-09-792-793A-10	Sequence 10, Appl
14	41	47.1	101	US-09-840-063-8	Sequence 8, Appl
15	41	47.1	145	US-09-768-826-60	Sequence 60, Appl
16	41	47.1	172	US-09-925-301-987	Sequence 987, Appl
17	41	47.1	203	US-09-768-826-41	Sequence 41, Appl
18	41	47.1	690	US-09-801-368-40	Sequence 40, Appl
19	41	47.1	867	US-09-992-598-84	Sequence 84, Appl

20	41	47.1	867	9	US-09-989-293A-84	Sequence 84, Appl
21	41	47.1	867	10	US-09-989-722-84	Sequence 84, Appl
22	41	47.1	867	10	US-09-989-723-84	Sequence 84, Appl
23	41	47.1	867	10	US-09-989-729-84	Sequence 84, Appl
24	41	47.1	867	10	US-09-989-727-84	Sequence 84, Appl
25	41	47.1	867	10	US-09-989-731-84	Sequence 84, Appl
26	41	47.1	867	10	US-09-989-732-84	Sequence 84, Appl
27	41	47.1	867	10	US-09-991-073-84	Sequence 84, Appl
28	41	47.1	867	10	US-09-990-442-84	Sequence 84, Appl
29	41	47.1	867	10	US-09-991-163-84	Sequence 84, Appl
30	41	47.1	867	10	US-09-993-604-84	Sequence 84, Appl
31	41	47.1	867	10	US-09-990-456-84	Sequence 84, Appl
32	41	47.1	867	10	US-09-989-721-84	Sequence 84, Appl
33	40	46.0	139	10	US-09-864-761-45901	Sequence 45901, A
34	39.5	45.4	389	10	US-09-835-788A-14	Sequence 14, Appl
35	35	44.8	80	10	US-09-916-790-10	Sequence 10, Appl
36	39	44.8	231	10	US-09-828-644-105	Sequence 105, App
37	39	44.8	695	10	US-09-792-127-2	Sequence 2, Appl
38	39	44.8	828	8	US-08-681-219-28	Sequence 28, Appl
39	39	44.8	829	10	US-09-792-127-5	Sequence 5, Appl
40	39	44.8	855	10	US-09-792-127-4	Sequence 4, Appl
41	38.5	44.3	917	10	US-09-808-743-10	Sequence 10, Appl
42	38.5	44.3	1019	10	US-09-801-574-76	Sequence 76, Appl
43	38	43.7	17	9	US-09-999-745-55	Sequence 55, Appl
44	38	43.7	17	9	US-09-554-000-39	Sequence 39, Appl
45	38	43.7	29	10	US-09-872-864-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-10-036-869-11  
Sequence 11, Application US/10036869  
Patent No. US20020151516A1  
GENERAL INFORMATION:  
APPLICANT: Mixson, James A  
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE THERAPY  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street, P.O. Box 2207  
City: Wilmington  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/036,869  
FILING DATE: 29-JUL-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,526  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/608,845  
FILING DATE: 16-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mc Morrow Jr., Robert G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 658-9141  
TELEFAX: (302) 658-5613  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-036-869-11

Query Match

Best Local Similarity 52.9%; Score 46; DB 12; Length 46;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AYYKFKKLLKSLKRL 17

Db 16 LYKFKKLLKSLKSL 32

RESULT 2

US-09-815-242-5696  
Sequence 5696, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

NUMBER OF SEQ ID NOS: 2001-02-16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5696

LENGTH: 439

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5696

Query Match

Best Local Similarity 49.4%; Score 43; DB 10; Length 439;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKLLKSLKRLG 18

Db 391 YAKFRDKLLDKLRMG 406

RESULT 3

US-09-822-263-14

Sequence 14, Application US/09822263

Patent No. US20020036598A1

GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas

APPLICANT: Vernet, Corine

APPLICANT: Shimkets, Richard A

APPLICANT: Burgess, Catherine

APPLICANT: Splytek, Kimberley

APPLICANT: Tchernev, Velizar T

TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded Th

FILE REFERENCE: 15966-572 CIP1

CURRENT APPLICATION NUMBER: US/09/822,263

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/672,665

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/156,745

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/158,942

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 60/159,248

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/169,344

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/215,048

PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 108

TYPE: PRT

ORGANISM: Homo sapiens

US-09-822-263-14

Query Match

Best Local Similarity 48.3%; Score 42; DB 10; Length 108;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKLLKSLK 13

Db 97 LYKFKKLLKSLK 108

RESULT 4

US-09-903-377-2

Sequence 2, Application US/09903377

Patent No. US20020116727A1

GENERAL INFORMATION:

APPLICANT: Allen, Keith D.

TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE

TITLE OF INVENTION: RECEPTOR 9A GENE DISRUPTIONS

FILE REFERENCE: R-365

CURRENT APPLICATION NUMBER: US/09/903,377

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/217,255

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/221,483

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: US 60/262,113

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 357

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Targeting vector

US-09-903-377-2

Query Match

Best Local Similarity 48.3%; Score 42; DB 10; Length 357;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKFKKLLKSLKRLG 18

Db 310 ERFRDVLKTLKMLG 324

RESULT 5

US-09-952-385-2

Sequence 2, Application US/09952385

Patent No. US20020119504A1

GENERAL INFORMATION:

APPLICANT: Andrew, David P.

```
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-952-385-2

Query Match      48.3%; Score 42; DB 10; Length 357;
Best Local Similarity 46.7%; Pred. No. 43;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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Db      310 EFRRLVTKLNKG 324

RESULT 6
US-10-000-759A-2
; Sequence 2, Application US/10000759A
; Patent No. US2002014191A1
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
; FILE REFERENCE: 1855.1064-003
; CURRENT APPLICATION NUMBER: US/10/000,759A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US/09/522,752
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: US 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-759A-2

Query Match      48.3%; Score 42; DB 12; Length 357;
Best Local Similarity 46.7%; Pred. No. 43;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      4 KKKKKLKSRLG 18
      :|:|:|:|:|:|:|
Db      310 EFRRLVTKLNKG 324

RESULT 7
US-09-767-215-2
; Sequence 2, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-142001
; CURRENT APPLICATION NUMBER: US/09/767,215
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; PRIOR FILING DATE: 2000-02-09
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1004
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-767-215-2

Query Match      48.3%; Score 42; DB 10; Length 1004;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db      929 EKKAKLKGLORLG 943

RESULT 8
US-09-767-215-5
; Sequence 5, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-142001
; CURRENT APPLICATION NUMBER: US/09/767,215
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-767-215-5

Query Match      48.3%; Score 42; DB 10; Length 1138;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4 KKKKKLKSRLG 18
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Db      978 EKKAKLKGLORLG 992

RESULT 9
US-09-765-614B-31
; Sequence 31, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klavness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Platelet
; OTHER INFORMATION: binding peptide
US-09-765-614B-31

Query Match      47.1%; Score 41; DB 10; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.3;
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Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKS 13  
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Db 2 LYKFKKKLKS 13

## RESULT 10

US-09-925-715-27  
; Sequence 27, Application US/09925715  
; Patent No. US20020102217A1  
; GENERAL INFORMATION:  
; APPLICANT: Nycomed Imaging AS  
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
; FILE REFERENCE: REF/KIavensess/206  
; CURRENT APPLICATION NUMBER: US/09/925,715  
; CURRENT FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 27  
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; SEQ ID NO 27  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Platelet  
US-09-925-715-27

Query Match 47.1%; Score 41; DB 10; Length 13;  
Best Local Similarity 75.0%; Pred. No. 2.3;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKS 13  
|||||  
Db 2 LYKFKKKLKS 13

## RESULT 11

US-10-036-869-9  
; Sequence 9, Application US/10036869  
; Patent No. US20020151516A1  
; GENERAL INFORMATION:  
; APPLICANT: Mixson, James A

TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA  
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
THERAPY  
NUMBER OF SEQUENCES: 43;  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Boye, Lodge, & Hutz  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 19899

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/036,869  
FILING DATE: 29-NO. US20020151516A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,526  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/608,845  
FILING DATE: 16-JUL-1996

ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 658-9141

TELEFAX: (302) 658-5613  
INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-036-869-9

Query Match 47.1%; Score 41; DB 12; Length 13;  
Best Local Similarity 75.0%; Pred. No. 2.3;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKS 13  
|||||  
Db 2 LYKFKKKLKS 13

## RESULT 12

US-09-792-793A-91  
; Sequence 91, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.  
; APPLICANT: Coggin, Philip  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
; FILE REFERENCE: 25020-601D  
; CURRENT APPLICATION NUMBER: US/09/792,793A  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Chemokine polypeptide: PF-4  
; PUBLICATION INFORMATION:  
; AUTHORS: Clark-Lewis et. al.,  
; JOURNAL: J. Leukoc. Biol.  
; VOLUME: 57  
; PAGES: 703-711  
; DATE: 1995  
US-09-792-793A-91

Query Match 47.1%; Score 41; DB 9; Length 70;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKS 13  
|||||  
Db 59 LYKFKKKLKS 70

## RESULT 13

US-09-229-304-10  
; Sequence 10, Application US/09229304  
; Patent No. US20020090671A1  
; GENERAL INFORMATION:  
; APPLICANT: TAM, Cheryl Shing  
; TITLE OF INVENTION: BONE STIMULATING FACTOR  
; FILE REFERENCE: 079997/0123  
; CURRENT APPLICATION NUMBER: US/09/229,304  
; CURRENT FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 09/048,058  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: PCT/CA96/00653  
; EARLIER FILING DATE: 1996-09-26  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 70

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemically  
OTHER INFORMATION: synthesized polypeptide  
US-09-229-304-10

Query Match 47.1%; Score 41; DB 10; Length 70;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13  
DB 59 LYKKIIRKLLS 70

RESULT 14  
US-09-940-063-8  
Sequence 8, Application US/09940063  
Patent No. US20020090657A1  
GENERAL INFORMATION:  
APPLICANT: Briskin, Michael J.  
APPLICANT: Murphy, Kristine E.  
APPLICANT: Wilbanks, Alyson M.  
APPLICANT: Wu, Lijun  
TITLE OF INVENTION: No. US20020090657A1e1 Antibodies and Ligands for "Bonzo"  
FILE REFERENCE: 1855,1070-000  
CURRENT APPLICATION NUMBER: US/09/940,063  
CURRENT FILING DATE: 2001-08-27  
PRIOR APPLICATION NUMBER: 09/449,437  
PRIOR FILING DATE: 1999-11-24  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-940-063-8

Query Match 47.1%; Score 41; DB 10; Length 101;  
Best Local Similarity 75.0%; Pred. No. 17;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13  
DB 90 LYKKIIRKLLS 101

RESULT 15  
US-09-768-826-60  
Sequence 60, Application US/09768826  
Patent No. US20020012966A1  
GENERAL INFORMATION:  
APPLICANT: Shi et al.  
TITLE OF INVENTION: 18 human secreted proteins  
FILE REFERENCE: P512P1  
CURRENT APPLICATION NUMBER: US/09/768,826  
CURRENT FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: PCT/US00/22350  
PRIOR FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: 60/148,759  
PRIOR FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 60  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-768-826-60

Query Match 47.1%; Score 41; DB 10; Length 145;  
Best Local Similarity 56.2%; Pred. No. 24;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 3 YKFKKKLLKSIRLG 18  
DB 65 YKEYKDKFGKSNKRG 80

Search completed: December 24, 2002, 09:19:01  
Job time : 10 secs

